IN THE CLAIMS:

Please amend the claims as follows:

1. (Original) A method for the diagnosis of a neonatal or infantile epilepsy syndrome as BFNIS in a patient with seizure onset in the first year of life, comprising testing for the presence of an alteration in the SCN2A gene, including in a regulatory region of the gene, in a patient sample, and establishing a diagnosis which will indicate a high probability of BFNIS when an SCN2A alteration is detected or establishing a diagnosis which will indicate a low probability of BFNIS when an SCN2A alteration is not detected.

2. (Original) A method as claimed in claim 1 wherein a diagnosis which will indicate a very high probability of BFNIS is established where the SCN2A alteration is known to be BFNIS associated.

3. (Original) A method as claimed in claim 1 wherein a diagnosis which will indicate a very high probability of BFNIS is established where the SCN2A alteration is present in the affected parent or relatives of the patient.

4. (Original) A method as claimed in claim 1 wherein a diagnosis which will indicate a very high probability of BFNIS is established where the SCN2A alteration is a missense mutation.

5. (Previously Presented) A method as claimed in claim 1 comprising performing one or more assays to test for the presence of an SCN2A alteration and to identify the nature of the alteration.

6. (Previously Presented) A method as claimed in claim 1 comprising:

(1) performing one or more assays to test for the presence of an alteration in the SCN2A gene of the patient; and, if the results indicate the presence of an alteration in the SCN2A gene,

(2) performing one or more assays to identify the nature of the SCN2A alteration.

7. (Previously Presented) A method as claimed in claim 1 further comprising testing for the presence of an alteration in the KCNQ2 and/or KCNQ3 genes, including in the regulatory regions of the genes, in a patient sample, and establishing a diagnosis which will indicate a high probability of BFNS when a KCNQ2 or KCNQ3 alteration is detected or establishing a diagnosis which will indicate a likelihood of BFIS when a KCNQ2 or KCNQ3 alteration is not detected.

8. (Original) A method for the diagnosis of a neonatal or infantile epilepsy syndrome as one of BFNIS, BFNS or BFIS in a patient with seizure onset in the first year of life comprising:

(1) (a) testing for the presence of an alteration in the SCN2A gene, including in a regulatory region of the gene, in a patient sample; and/or

(b) testing for the presence of an alteration in the KCNQ2 and/or KCNQ3 genes, including in regulatory regions of the genes, in the patient sample; and

(2) (a) establishing a diagnosis which will indicate a high probability of BFNIS when an SCN2A alteration is detected;

(b) establishing a diagnosis which will indicate a high probability of BFNS when a KCNQ2 or KCNQ3 alteration is detected; or

(c) establishing a diagnosis which will indicate a likelihood of BFIS when an SCN2A, KCNQ2 or KCNQ3 alteration is not detected.

9. (Original) A method as claimed in claim 8 comprising performing one or more assays to test for the presence of an SCN2A, KCNQ2 and/or KCNQ3 alteration and to identify the nature of the alteration.

10. (Original) A method as claimed in claim 8 comprising:

(1) performing one or more assays to test for the presence of an alteration in the SCN2A, KCNQ2 and/or KCNQ3 genes of the patient; and, if the results indicate the presence of an alteration in any one of these genes,

(2) performing one or more assays to identify the nature of the alteration.

11. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays is a DNA ~~hybridisation~~ hybridization assay.

12. (Currently amended) A method as claimed in claim 11 wherein an SCN2A, KCNQ2 or KCNQ3 gene probe, an SCN2A, KCNQ2 or KCNQ3 exon-specific probe, or an SCN2A, KCNQ2 or KCNQ3 allele specific probe is ~~hybridised~~ hybridized to genomic DNA isolated from said patient.

13. (Currently amended) A method as claimed in claim [[1]] 5 wherein one of the assays is high performance liquid chromatography.

14. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays is an electrophoretic assay.

15. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays comprises analysis of SCN2A, KCNQ2 or KCNQ3 genes from a sample DNA from the patient, wherein the sample DNA to be tested is quantitatively amplified for at least one exon of the SCN2A, KCNQ2 or KCNQ3 genes to produce amplified fragments and the length of the amplification products for each amplified exon is compared to the length of the amplification products obtained when a wild-type SCN2A, KCNQ2 or KCNQ3 gene is amplified using the same primers, whereby differences in length between an amplified sample exon and the corresponding amplified wild-type exon reflect the occurrence of a truncating alteration in the sample SCN2A, KCNQ2 or KCNQ3 gene.

16. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays incorporates DNA amplification using SCN2A, KCNQ2 or KCNQ3 allele specific oligonucleotides.

17. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays is SSCP analysis.

18. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays is RNase protection.

19. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays is DGGE.

20. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays is an enzymatic assay.

21. (Currently amended) A method as claimed in claim 20 wherein said enzymatic assay incorporates the use of MutS.

22. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays examines the electrophoretic mobility of the SCN2A, KCNQ2 or KCNQ3 proteins of the patient.

23. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays is an immunoassay.

24. (Currently amended) A method as claimed in claim [[4]] 5 wherein one of the assays is DNA sequencing.

25. (Original) A method for testing patients for BFNIS-associated mutations in the SCN2A gene comprising the steps of:

a) quantitatively amplifying at least one exon of the SCN2A gene from a body sample of each patient to produce amplified fragments;

b) comparing the properties of the amplified fragments to standard values based upon the fragments produced by amplification of the same exon in a non-mutant SCN2A gene; and

c) determining the nucleic acid sequence of each exon identified in b) that has different properties in the patient compared to the corresponding non-mutant SCN2A exon.

26. (Original) A method for testing patients for BFNIS-associated mutations in the SCN2A gene comprising the steps of:

a) quantitatively amplifying, from a body sample of each patient at least one exon of the SCN2A gene using primers complementary to intron regions flanking each amplified exon;

b) comparing the length of the amplification products for each amplified exon to the length of the amplification products obtained when a wild-type SCN2A gene is amplified using the same primers, whereby differences in length between an amplified sample exon and the corresponding amplified wild-type exon reflect the occurrence of a truncating mutation in the sample SCN2A gene; and

c) determining the nucleic acid sequence of each exon identified in b) to contain a truncating mutation.

27. (Currently amended) A method for testing patients for BFNIS-associated mutations in the SCN2A gene comprising the steps of:

a) quantitatively amplifying, from a body sample of each patient at least one exon of the SCN2A gene using primers complementary to intron regions flanking each amplified exon;

b) hybridizing ~~hybridising~~ the fragments from a) with fragments produced by amplification of the same exon in a non-mutant SCN2A gene;

c) determining the nucleic acid sequence of each patient exon identified in b) that either does not hybridize ~~hybridise~~ to corresponding wild-type fragments or forms a mismatched heteroduplex.